

GenCore version 4.5  
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OM protein - protein search, using sw model

February 11, 2002, 13:31:13 ; Search time 27.64 Seconds  
(without alignments)  
1725.209 Million cell updates/sec

Title: US-09-553-431-2  
Perfect score: 1654  
Sequence: 1 MASLRFTSTNHSLLPSSL.....KAVMEERPKRGFFSPFGC 326

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

\* Database :  
1: SPREMBL\_17:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phase:\*  
11: sp\_plant:\*  
12: sp\_rhodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID     | Description        |
|------------|--------|-------------|--------|-----------|--------------------|
| 1          | 1654   | 100.0       | 326    | 10 Q9MBA2 | Q9MBA2 Arabidopsis |
| 2          | 1175.5 | 71.1        | 295    | 10 Q9FV40 | Q9FV40 Tagetes ere |
| 3          | 1067.5 | 64.5        | 306    | 10 Q9LWY6 | Q9LWY6 oryza sativ |
| 4          | 756    | 45.7        | 274    | 8 Q9R3P6  | Q9R3P6 nephriselm  |
| 5          | 752    | 45.5        | 359    | 8 Q9R3P6  | Q9R3P6 nephriselm  |
| 6          | 573.5  | 34.7        | 276    | 2 Q9RMB7  | Q9RMB7 delnococ    |
| 7          | 536.5  | 32.4        | 264    | 2 Q9K8H9  | Q9K8H9 bacillus ha |
| 8          | 516    | 31.2        | 262    | 2 Q67033  | Q67033 aquilex aeo |
| 9          | 514.5  | 31.1        | 269    | 2 Q9PD08  | Q9PD08 xyella fas  |
| 10         | 480.5  | 29.1        | 271    | 2 Q9HYZ6  | Q9HYZ6 pseudomonas |
| 11         | 479    | 29.0        | 179    | 10 Q9SPPO | Q9SPPO oryza sativ |
| 12         | 468    | 28.3        | 276    | 2 Q9KQ8   | Q9KQ8 vibrio chol  |
| 13         | 449.5  | 27.2        | 271    | 2 Q9Q0Y6  | Q9Q0Y6 neisseria m |
| 14         | 449.5  | 27.2        | 271    | 2 Q9AG19  | Q9AG19 neisseria g |
| 15         | 366    | 22.1        | 260    | 1 Q9V165  | Q9V165 pyrococcus  |
| 16         | 344.5  | 20.8        | 259    | 1 Q27868  | Q27868 methanobact |
| 17         | 341.5  | 20.6        | 245    | 1 Q58346  | Q58346 pyrococcus  |
| 18         | 335    | 20.3        | 263    | 1 Q29562  | Q29562 archaeoglob |
| 19         | 327.5  | 19.8        | 245    | 1 Q9UY50  | Q9UY50 pyrococcus  |

|    |       |      |     |          |                    |
|----|-------|------|-----|----------|--------------------|
| 20 | 266   | 16.1 | 252 | 1 Q59470 | Q59470 pyrococcus  |
| 21 | 262.5 | 15.9 | 305 | 1 Q9HNP1 | Q9HNP1 halobacteri |
| 22 | 254   | 15.4 | 217 | 1 Q59249 | Q59249 pyrococcus  |
| 23 | 250   | 15.1 | 319 | 2 Q9L775 | Q9L775 xanthomonas |
| 24 | 249   | 15.1 | 280 | 2 Q9RGE0 | Q9RGE0 pseudomonas |
| 25 | 247.5 | 15.0 | 251 | 1 Q9VIR2 | Q9VIR2 pyrococcus  |
| 26 | 246.5 | 14.9 | 288 | 2 Q9KAS4 | Q9KAS4 bacillus ha |
| 27 | 243.5 | 14.7 | 323 | 1 Q9HOY5 | Q9HOY5 halobacteri |
| 28 | 241   | 14.6 | 268 | 2 Q9P756 | Q9P756 campylobact |
| 29 | 239.5 | 14.5 | 304 | 2 Q56340 | Q56340 treponema p |
| 30 | 238.5 | 14.4 | 295 | 2 Q44911 | Q44911 borrelia bu |
| 31 | 238   | 14.4 | 112 | 2 Q9AENS | Q9AENS burkholderi |
| 32 | 236.5 | 14.3 | 281 | 2 Q44757 | Q44757 borrelia bu |
| 33 | 236   | 14.3 | 275 | 2 Q87380 | Q87380 pseudomonas |
| 34 | 230   | 13.9 | 294 | 2 Q25678 | Q25678 helicobacte |
| 35 | 228   | 13.8 | 313 | 2 Q9K0D3 | Q9K0D3 vibrio chol |
| 36 | 227   | 13.7 | 295 | 2 Q9L816 | Q9L816 vibrio para |
| 37 | 224   | 13.5 | 294 | 2 Q9ZM33 | Q9ZM33 helicobacte |
| 38 | 218   | 13.2 | 273 | 2 Q9Z557 | Q9Z557 zymomonas m |
| 39 | 209.5 | 12.7 | 378 | 2 Q83825 | Q83825 treponema p |
| 40 | 204.5 | 12.4 | 278 | 2 Q67267 | Q67267 aquilex aeo |
| 41 | 202   | 12.2 | 297 | 1 Q9VOC7 | Q9VOC7 pyrococcus  |
| 42 | 197   | 11.9 | 300 | 1 Q58711 | Q58711 pyrococcus  |
| 43 | 196.5 | 11.9 | 295 | 1 Q9VOD9 | Q9VOD9 pyrococcus  |
| 44 | 196   | 11.9 | 382 | 2 Q9KT68 | Q9KT68 vibrio chol |
| 45 | 195   | 11.8 | 288 | 2 Q9X117 | Q9X117 thermotoga  |

## ALIGNMENTS

RESULT 1  
ID Q9MBA2 PRELIMINARY; PRT; 326 AA.  
AC Q9MBA2;  
DT 01-OCT-2000 (TREMUREL.15, Created)  
DT 01-OCT-2000 (TREMUREL.15, Last sequence update)  
DT 01-JUN-2001 (TREMUREL.17, Last annotation update)  
DE MIND (SEPTUM SITE-DETERMINING MIND).  
GN MIND.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RX MEDLINE=98290546; PubMed=9628582;  
RA Sato S., Kaneko T., Kocani H., Nakamura Y., Asamizu E., Miyajima N.,  
RA Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.  
RT Sequence features of the regions of 1,456,315 bp covered by nineteen  
RT physically assigned P1 and TAC clones.";  
RL DNA Res. 5:41-54 (1998).  
DR EMBL: AB030278; BAA90261.1; -  
DR EMBL: AB009056; BAB08725.1; -  
DR InterPro: IPR000707; Para.  
DR Pfam: PFC0991; Para.1  
SQ SEQUENCE 326 AA; 35690 MW; BE7AEF4307167825 CRC64;

Query Match 100.0%; Score 1654; DB 10; Length 326;  
Best Local Similarity 100.0%; Pred. No. 2.1e-118;  
Matches 326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MASLRFTSTNHSLLPSSLKTLISSPRFVNSRRSPRSVLOFNKRPPLAGTPT 60  
|||||

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Db 1 MASRLSTNHOSLLPSSLSOKTLISSPRFVNPNRSRSPKRSVLQFNKRPPELAGETPRI 60
QY 61 VITSGKGVGKTTTANGLIARYGFSVAIDADLGRNLDLGLLENRVNYTCVEYI 120
    |||
Db 61 VVITSGKGVGKTTTANGLIARYGFSVAIDADLGRNLDLGLLENRVNYTCVEYI 120
QY 121 NGCDRLDQALVDRKWSNFELLCISPRSKLPMGFGKALEWLVDAKTRPEGSPDFIT 180
    |||
Db 121 NGCDRLDQALVDRKWSNFELLCISPRSKLPMGFGKALEWLVDAKTRPEGSPDFIT 180
QY 181 DCPAGIAGFTTATPANEAVALVTPPTITLADADRVYGLLECDGIRDKIMVNRVTRTM 240
    |||
Db 181 DCPAGIAGFTTATPANEAVALVTPPTITLADADRVYGLLECDGIRDKIMVNRVTRTM 240
QY 241 IKGDMMSVLDVQEMGLSLGLVPEDESEVIRKSTNRGFPVLNKPPTLAGLAFEOAAMRL 300
    |||
Db 241 IKGDMMSVLDVQEMGLSLGLVPEDESEVIRKSTNRGFPVLNKPPTLAGLAFEOAAMRL 300
QY 301 VEODSMKAVVEEPPKRGFFSFGG 326
    |||
Db 301 VEODSMKAVVEEPPKRGFFSFGG 326

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RESULT 2
Q9FV40 PRELIMINARY; PRT; 295 AA.
AC Q9FV40;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE MIND.
OS Tagetes erecta (African marigold).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Tagetes.
OC NCBI_TaxID=13708;
RN [1]
RP SEQUENCE FROM N.A.
RT Moehs C.P., Tian L., DellaPenna D.;
RT "Analysis of carotenoid biosynthetic gene expression during marigold
RT petal development.";
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: ACP251019; AAG10431.1; -.
DR InterPro: IPR000707; Para.
DR Pfam: PF00991; Para: 1.
SQ SEQUENCE 295 AA; 32756 MW; 212BD476BF58747F CRC64;

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Query Match 71.1%; Score 1175.5; DB 10; Length 295;  
 Best Local Similarity 72.0%; Pred. No. 6e-82;  
 Matches 247; Conservative 15; Mismatches 16; Indels 65; Gaps 7;

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QY 1 MASRLSTNHOSLLPSSLSOKTLISSPRFVN-NPSRRS-----PIRSVLQ 46
    |||
Db 1 MTSIRF-----LTSPVLCSSITPTNPPLKTKLPKPKYPPKPPKRSVLQ 47
    |||
QY 47 FNKKPELAGETPRIVITSGKGVGKTTTANGLIARYGFSVAIDADLGRNLDL 106
    |||
Db 48 YNKKPELAGETPR-----VAIDADVGLRNLDDL 77
    |||
QY 107 GLENRVNYTCVEYINGCDRLDQALVDRKWSNFELLCISPRSKLPMGFGKALEWLVDA 166
    |||
Db 78 GLENRVNYTCVEYINGCDRLDQALVDRKWSNFELLCISPRSKLPMGFGKALEWLVDA 136
    |||
QY 167 LKTRPEGSPDFITIDCPAGIAGFTTATPANEAVALVTPPTITLADADRVYGLLECDGI 226
    |||
Db 137 LKTRPEGSPDFITIDCPAGIAGFTTATPANEAVALVTPPTITLADADRVYGLLECDGI 196
    |||
QY 227 RDKIMVNRVTRTMIKGDMMSVLDVQEMGLSLGLVPEDESEVIRKSTNRGFPVLN 283
    |||
Db 197 RDKIMVNRVTRTMIKGDMMSVLDVQEMGLSLGLVPEDESEVIRKSTNRGFPVLN 252

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QY 284 KPPTLAGLAFEOAAMRLVEODSMKAVVEEPPKRGFFSFGG 326
    |||
Db 253 KPPTLAGLAFEOAAMRLVEODSMKAVVEEPPKRGFFSFGG 295
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RESULT 3
Q9LWY6 PRELIMINARY; PRT; 306 AA.
AC Q9LWY6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE SIMILAR TO CHLORELLA VULGARIS C-27 CHLOROPLAST DNA.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone: p0644B06.";
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP001129; BAA90628.1; -.
DR InterPro: IPR000707; Para.
DR Pfam: PF00991; Para: 1.
SQ SEQUENCE 306 AA; 32341 MW; CECAB38219512690 CRC64;

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Query Match 64.5%; Score 1067.5; DB 10; Length 306;  
 Best Local Similarity 68.4%; Pred. No. 1.1e-73;  
 Matches 216; Conservative 31; Mismatches 50; Indels 19; Gaps 5;

```

QY 14 LILPSSLSOKTLISSPRFVNPNRSRSPKRSVLQFNKRPPELAGETPRIVITSGKGVGKT 73
    |||
Db 7 LILPS-----RCPPASSPARHGG-----RTAPELSGPPRVVYVITSGKGVGKT 51
    |||
QY 74 TTTANGLIARYGFSVAIDADLGRNLDLGLLENRVNYTCVEYINGCDRLDQALVDR 133
    |||
Db 52 TTTANGLIARYGFSVAIDADLGRNLDLGLLENRVNYTCVEYINGCDRLDQALVDR 111
    |||
QY 134 KRWNSFELLCISPRSKLPMGFGKALEWLVDAKTRPEGSPDFITIDCPAGIAGFTTA 193
    |||
Db 112 RALHDLQLCLISPRSKLPMGFGKALEWLVDAKTRPEGSPDFITIDCPAGIAGFTTA 170
    |||
QY 194 IMPANEAVLVTPPTITLADADRVYGLLECDGIRDKIMVNRVTRTMIKGDMMSVLDVQ 253
    |||
Db 171 IAPAEAVLVTPPTITLADADRVYGLLECDGIRDKIMVNRVTRTMIKGDMMSVLDVQ 230
    |||
QY 254 EMGLSLGLVPEDESEVIRKSTNRGFPVLNKPPTLAGLAFEOAAMRLVEODSMKAVVEE 313
    |||
Db 231 EMGLSLGLVPEDESEVIRKSTNRGFPVLNKPPTLAGLAFEOAAMRLVEODSMKAVVEE 290
    |||
QY 314 E-PKRR-GFFSFGG 326
    |||
Db 291 QERPKKAGFFSFGG 306
    |||

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RESULT 4
Q9T3P6 PRELIMINARY; PRT; 274 AA.
AC Q9T3P6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE SEPTUM-SITE DETERMINING PROTEIN.
GN MIND.
OS Nephroselmis olivacea.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
OC Chlorodendreales; Chlorodendraceae; Nephroselmis.

```

OX NCBI\_TaxID=31312;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9938694; PubMed=10468594;  
 RA Turnell M., Ollis C., Lemieux C.;  
 RT "The complete chloroplast DNA sequence of the green alga *Nephroselmis*  
 RT *olivaeca*: insights into the architecture of ancestral chloroplast  
 RT genomes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).  
 RP [2]  
 RN SEQUENCE FROM N.A.  
 RA Turnell M., Ollis C., Lemieux C.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF137379; AAD54908.1;  
 DR EMBL; AF137379; AAD54881.1;  
 DR InterPro; IPR000707; Para.  
 DR Pfam; PF00991; Para; 1.  
 DR Chloroplast.  
 KM SEQUENCE 274 AA; 30126 MW; 9D0A1449E6815845 CRC64;

Query Match

Best Local Similarity 45.7%; Score 756; DB 8; Length 274;  
 Matches 155; Conservative 39; Mismatches 60; Indels 10; Gaps 3;

OY 59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIDADGLRNDLLGLLENRVNTCVE 118  
 DB 14 RIVVITSGKGVGKTTATNGLARGLRVALIDADIGLRNDLLGLLENRVNTAME 73  
 OY 119 VINGDRLDQALVDRKMSNFELLCISPRSKLPMFGGKALEMVLDAKTRPGSPDFI 178  
 DB 74 VIEGOCRLQALIRDRKMSNFELLCISPRSKLPMFGGKALEMVLDAKTRPGSPDFI 128  
 OY 179 IIDCAGTADGTTATTPANEAVLVTPTALRDADRVTLGECGDIRDKIMVNVRT 238  
 DB 129 IIDCAGTADGTTATTPANEAVLVTPTALRDADRVTLGECGDIRDKIMVNVRT 188  
 OY 239 DMKGEDMMSVLDVOMELSLGLVSEVIRSTNRGFPVLPKPTAGLAFQDAW 298  
 DB 189 EMIQNDMMSVLDVOMELSLGLVSEVIRSTNRGFPVLPKPTAGLAFQDAW 248  
 OY 299 RIVEDSKMAVNEEPRKRGFS 322  
 DB 249 RLVGLPS-----PSDSAPSRGWFA 267

RESULT 5  
 OY 59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIDADGLRNDLLGLLENRVNTCVE 118  
 DB 14 RIVVITSGKGVGKTTATNGLARGLRVALIDADIGLRNDLLGLLENRVNTAME 73  
 OY 119 VINGDRLDQALVDRKMSNFELLCISPRSKLPMFGGKALEMVLDAKTRPGSPDFI 178  
 DB 74 VIEGOCRLQALIRDRKMSNFELLCISPRSKLPMFGGKALEMVLDAKTRPGSPDFI 128  
 OY 179 IIDCAGTADGTTATTPANEAVLVTPTALRDADRVTLGECGDIRDKIMVNVRT 238  
 DB 129 IIDCAGTADGTTATTPANEAVLVTPTALRDADRVTLGECGDIRDKIMVNVRT 188  
 OY 239 DMKGEDMMSVLDVOMELSLGLVSEVIRSTNRGFPVLPKPTAGLAFQDAW 298  
 DB 189 EMIQNDMMSVLDVOMELSLGLVSEVIRSTNRGFPVLPKPTAGLAFQDAW 248  
 OY 299 RIVEDSKMAVNEEPRKRGFS 322  
 DB 249 RLVGLPS-----PSDSAPSRGWFA 267

AC 09JUR6 PRELIMINARY; PRT: 359 AA.  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE CELL DIVISION INHIBITOR MIND.  
 GN MIND.  
 OS *Prothoea wickerhamii*.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;  
 OC Chlorellaceae; Prothoea.  
 OX NCBI\_TaxID=3111;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Knauf U., Hachtel W.;  
 RT "A 22 kb fragment of the 53 kb plastid genome of the colourless alga  
 RT *Prothoea wickerhamii* containing atp-, rpl-, rps-, rrr-, and trn-  
 RT genes.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ245645; CAB53105.1;  
 DR InterPro; IPR000707; Para.  
 DR Pfam; PF00991; Para; 1.  
 DR Cell division; Chloroplast.  
 KM SEQUENCE 359 AA; 40804 MW; E550EAF50BC0A51E CRC64;

Query Match  
 Best Local Similarity 45.5%; Score 752; DB 8; Length 359;  
 Matches 159; Conservative 44; Mismatches 62; Indels 22; Gaps 5;

OY 35 PSRRSPRSVL-QFNRP-----ELAGE-----IPRIVITSGKGVGKTTT 77  
 DB 53 PEERKITEQLQKPSSESEVNTLDELKGDSELEPRVITSGKGVGKTTT 112  
 OY 78 NGLSLARYGSVAIDADGLRNDLLGLLENRVNTCVEVINGDRLDQALVDRKMS 137  
 DB 113 NGLSLARYGSVAIDADGLRNDLLGLLENRVNTCVEVINGDRLDQALVDRKMS 172  
 OY 138 NEELCISPRSKLPMFGGKALEMVLDAKTRPGSPDFIIDCPAGIDGTTATTPA 197  
 DB 173 NGLAVSKNHOK--YVNGQHMRLVFSIK---ELGINSILDCPAGIDGTTATTPA 227  
 OY 198 NEAVLVTPTDITRALRDADRVTLGECGDIRDKIMVNVRTDMKGEDMMSVLDVOMELG 257  
 DB 228 NEAVLVTPTDITRALRDADRVTLGECGDIRDKIMVNVRTDMKGEDMMSVLDVOMELG 287  
 OY 258 LSLGLVPEDESEVIRSTNRGFPVLPKPTAGLAFQDAWRLVED 304  
 DB 288 IPLGLPDTNVITSTNKGPELVLDKLTLSIAFENMARRLIGE 334

RESULT 6

OY 59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIDADGLRNDLLGLLENRVNTCVE 118  
 DB 14 RIVVITSGKGVGKTTATNGLARGLRVALIDADIGLRNDLLGLLENRVNTAME 73  
 OY 119 VINGDRLDQALVDRKMSNFELLCISPRSKLPMFGGKALEMVLDAKTRPGSPDFI 178  
 DB 74 VIEGOCRLQALIRDRKMSNFELLCISPRSKLPMFGGKALEMVLDAKTRPGSPDFI 128  
 OY 179 IIDCAGTADGTTATTPANEAVLVTPTALRDADRVTLGECGDIRDKIMVNVRT 238  
 DB 129 IIDCAGTADGTTATTPANEAVLVTPTALRDADRVTLGECGDIRDKIMVNVRT 188  
 OY 239 DMKGEDMMSVLDVOMELSLGLVSEVIRSTNRGFPVLPKPTAGLAFQDAW 298  
 DB 189 EMIQNDMMSVLDVOMELSLGLVSEVIRSTNRGFPVLPKPTAGLAFQDAW 248  
 OY 299 RIVEDSKMAVNEEPRKRGFS 322  
 DB 249 RLVGLPS-----PSDSAPSRGWFA 267

AC 09JUR6 PRELIMINARY; PRT: 276 AA.  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE SEPTUM SITE-DETERMINING PROTEIN.  
 GN DR0752.  
 OS *Deinococcus radiodurans*.  
 OC Bacteria; Thermus; Deinococcus group; Deinococcales; Deinococcus.  
 OX NCBI\_TaxID=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=RI.  
 RX MEDLINE=20036896; PubMed=10567266;  
 RA White O., Eison J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
 RA McFate K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Vamathevan J.J., Lam P., McDonald L., Uitterback T., Zaleski C.,  
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Genome sequence of the radioresistant bacterium *Deinococcus*  
 RT *radiodurans* RI.";  
 RL Science 286:1571-1577(1999).  
 DR EMBL; AE001931; AAF10331.1;  
 DR TIGR; DR0752;  
 DR InterPro; IPR000392; NitrogenaseII.  
 DR InterPro; IPR000707; Para.  
 DR Pfam; PF00142; fer4\_NiFeH; 1.  
 DR Pfam; PF00991; Para; 1.  
 KM Complete proteome.  
 SO SEQUENCE 276 AA; 29420 MW; AD74FDFCA5820DOC CRC64;

Query Match  
 Best Local Similarity 44.3%; Score 573.5; DB 2; Length 276;  
 Matches 125; Conservative 52; Mismatches 72; Indels 33; Gaps 5;

OY 59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIDADGLRNDLLGLLENRVNTCVE 118  
 DB 12 RIVVITSGKGVGKTTTANVGLSLARYGSVAIDADGLRNDLLGLLENRVNTCVE 71  
 OY 119 VINGDRLDQALVDRKMSNFELLCISPRSKLPMFGGKALEMVLDAKTR----- 170

|                           |  |   |     |
|---------------------------|--|---|-----|
| Dd                        | 72   | VLEGCRRNOLILDKRRENHLLPAQSTRNK-----DALDEVEKKEYVKG                | 117 |
| Qy                        | 171  | --PEGSPDFIIIDCPAGIADGFTAITPANEAIVLTPPDITALDADRVYGLLEDGIRD       | 228 |
|                           |  | : :           : :       : :   : :           : :   :             |     |
| Dd                        | 118  | LLEEGRFRLVDISPAGIEGSGRTAAAPAEALAVVNEEVSVDADRILIGLLEAQOITE       | 177 |
| Qy                        | 229  | IKMIYNRYRTMIMGEDMMASVLDOEMGLSLGVIPDSSEVIRSTNGFPFLYANKPPTL       | 288 |
|                           |  | [::: :: ::  : : :   : : :   : : :   : : :   : : :   : : :       |     |
| Dd                        | 178  | IRLVNRYLRPRKMVASGNMLSTIDMDWDLIGVAPRIGVIPPEDEBIYSTINGGEVAVGK--TK | 235 |
| Qy                        | 289  | AGLAFEQAAMRLVEDODSMKAVAVEEPKRGGFFS---FFCG                       | 326 |
|                           |  | : :   : :   : :   : :   : :   : :   : :   : :                   |     |
| Dd                        | 236  | AGDAFMATAORIQQDVDPFKLTREE--KGIWAIRLRFGG                         | 274 |
| RESULT                    | 7  |   |     |
| O9K8H9                    |  | PRELIMINARY; PRT; 264 AA.                                       |     |
| AC                        | O9K8H9;  |   |     |
| ID                        | O9K8H9;  |   |     |
| DT                        | 01-OCT-2000 (TREMBLrel. 15, Created)                                 |   |     |
| Pt                        | 01-OCT-2000 (TREMBLrel. 15, Last sequence update)                    |   |     |
| Df                        | 01-JUN-2001 (TREMBLrel. 17, last annotation update)                  |   |     |
| DE                        | SEPUM SITE DETERMINING PROTEIN.                                      |   |     |
| DN                        | MIND OR BH3027.  |   |     |
| OS                        | Bacillus halodurans.   |   |     |
| OC                        | Bacteria; Firmicutes; Bacillus/Clostridium group;                    |   |     |
| CC                        | Bacillus/Staphylococcus group; Bacillus.                             |   |     |
| OX                        | NCBI_TaxId=86665;  |   |     |
| RN                        | [1]  |   |     |
| RP                        | SEQUENCE FROM N.A.   |   |     |
| RC                        | STRAIN-C-125 / JCM 9153;   |   |     |
| RX                        | MEDLINE=20512582; PubMed=11058132;                                   |   |     |
| RA                        | Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,    |   |     |
| KA                        | Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,            |   |     |
| HA                        | Horiuchi K.;   |   |     |
| RT                        | "Complete genome sequence of the alkaliphilic bacterium Bacillus     |   |     |
| RL                        | halodurans and genomic sequence comparison with Bacillus subtilis."; |   |     |
| Nucleic Acids Res.        | 28:4317-4331(2000).  |   |     |
| DR                        | EMBL; AF001517; BAB06746.1; -  |   |     |
| DR                        | InterPro; IPR000392; NitrogenaseII.                                  |   |     |
| DR                        | InterPro; IPR000707; Para.   |   |     |
| DR                        | pfam; PF00142; fer4_N1FH.1.  |   |     |
| DR                        | pfam; PF00991; Para; 1.  |   |     |
| KW                        | Complete proteome.   |   |     |
| SQ                        | SEQUENCE 264 AA; 28818 MW; 78D523BE583172F CRC64;                    |   |     |
| Query Match               | 32.4%; Score 536.5; DB 2; Length 264;                                |   |     |
| Best Local Similarity     | 41.1%; Pred. No. 2.9e-33;  |   |     |
| Matches 109; Conservative | 66; Mismatches 83; Indels 7; Gaps 3                                  |   |     |
| Qy                        | 61   | VVTSSKGCGKTTTANVLSLARGFSVATDADLGRLNDLLGLENRVNYTCVEVI            | 120 |
|                           |  | : :           : :       : :   : :           : :   :             |     |
| Dd                        | 5  | IYTSGGCVGKTTTSNIGTALALSGKKVCVLDTDIGRLNDVYVAGLERRIITYDLVDVY      | 64  |
| Qy                        | 121  | NGDCRLDQALVVRDKRMSNFELCISKPRSXLPMGFCGKALEWLVDALKTRPEGSPDFII     | 180 |
|                           |  | : :   : :   : :   : :   : :   : :   : :   : :                   |     |
| Dd                        | 65   | EGRCKRLKQALIKRKRFECNLPLPAQCRKD--SAVTPEQMKETIVEELKO---EYDYVLI    | 118 |
| Qy                        | 181  | DCPAGIDAGITTATTAPANEAIVLTPDITLRLRADRYTGILLEDDGIRDIKMIYNRYRTM    | 240 |
|                           |  | : :   : :           : :         : :   : :                       |     |
| Dd                        | 119  | DCPAGIEGCFKNVAVAGADKAIAVTPPEISSVRADRIIGLLEKEEVAPRLVNRIIGHA      | 178 |
| Qy                        | 241  | IKGDMMASVLDOEMGLSLGVIPDESSEVIRSTNGFPFLYANKPPTLAGLAFEQAAMRL      | 300 |
|                           |  | : :   : :   : :   : :   : :   : :   : :   : :   : :   : :       |     |
| Dd                        | 179  | MKMGEMADVDEIYSITALELGIYVDENENIKSNKEPIALH-PDSKASVAIRNLARI        | 237 |
| Qy                        | 301  | VEODSMKAVAVEEPKRGGFFSFFG  | 325 |
|                           |  | : : : : :   : :   : :   : :   : :   : :   : :   : :             |     |
| Dd                        | 238  | LGFTVPLMSPQEKGVLAKIKSFPG  | 262 |
| RESULT                    | 8  |   |     |

[illegible]

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Query Match      29.1%, Score 480.5; DB 2: Length 271;
Best Local Similarity 39.6%, Pred. No.5,6e-29;
Matches 113; Conservative 54; Mismatches 83; Indels 35; Gaps
7;

QY      59 RIVVITSKGGVCKTTTANVNGLSIARGFSVVAIDADLGLRNLDDLGLGNRVVITCYE 118
Db      3 KLVVTSKGGGKTKTTTAAIGTALGFKVIVDFVGLNLDLIMGCERRVVAIDVFN 62
QY      119 VINGCDRLDQALVDRKMSNFELLCISKPRSKLPMGFGKALEMLVDAL-----KTRPE 172
Db      63 VVNGEVTTLQALLKKRLLENLHVLAASQTRDK-----DALTKRGVEKVMAE 108
QY      173 GSPDF--IIIDCPAIDAGFITAITPAEVAIVYTPDITALLADARVNGLECDGIRDK 230
Db      109 LRKDEYITICSPAGIEGAILAMFAEADIVATVPEVSSVNDSDRMGLASKSQRAEK 168
QY      231 -----MIVNRVTTDIKIGEDMMSVLDVDEMLGSLGVPEDESEVYIRSTNRGFPVL 282
Db      169 GEEPIKEHLLTRYPERVHTGEMGLVDVDEILIRLGVIPESQAVYKASNGCVPTL 228
QY      283 NKRPPLAGLAFEOAMRLVVEDSMKAVVVEEPPKRGFS--FFG 326
Db      229 DEQSD-AGQATSDAVDRLGKETIPRFL---DYQKKGFLQRLFGG 269

RESULT 11
Q9SPPO PRELIMINARY; PRT; 179 AA.
Q9SPPO:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CELL DIVISION INHIBITOR MIND HOMOLOG (FRAGMENT).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eihartoideae; Oryzaeae; Oryza.
OX NCBI_Taxid=4530;
NN 11
PP SEQUENCE FROM N.A.
RC STRAIN=CV, IR-BB21;
RA Han F., Killian A., Chen J.P., Kudrna D., Steffenson B., Yamamoto K.,
RA Matsunoto T., Sasaki T., Kleinholz A.;
RT "Sequence analysis of a rice BAC covering the syntenous barley Rpg1
RT region.";
RL Genome 0:0-0.0(1999).
DR EMBL; AF149810; AA:00142.1; -
DR InterPro; IPR000392; NITrogenaseII.
OR Pfam; PF00142; fer4_NiH; 1.
KW Cell division.
FT NON_TER 179 179
SQ SEQUENCE 179 AA; 18705 MW; 3DE6FAF7DAE76E77 CRC64;

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Query Match 29.0%; Score 479; DB 10: Length 179;  
Best Local Similarity 57.1%; Pred. No. 4.1e-29;  
Matches 100; Conservative 19; Mismatches 40; Indels 16; Gaps 3;

QY 14 LLLPSSLSOKTLLISSPFRVNNPSRRSPRLSVLQENRKPBLAGEPRIVITSGKGVGKT 73  
DB 7 LLLPSS-----RCPPEASSPARHG-----RTAPELSGPRVAVVITSGKGVGKT 51  
QY 74 TTTANVGLSLARIGFVVAIDADGLRNLDDLGLERNVANTCEVINGDCRLDALVRD 133  
DB 52 TTTANLAASLARISLSAVADADAGLRNLDDLGLERNVANTCEVINGDCRLDALVRH 111  
QY 134 KRNSFELLICISPRSKLPMFGGKALEMLVDALKTREGSPDFTIIDCPAGIDA 188  
DB 112 RALHDLQLLSLSKRSLPLAFSGSKLTWADALR-RAANPAPFLIDCPAGQSA 165

RESULT 12  
Q9K0N8 PRELIMINARY; PRT; 276 AA.  
AC Q9K0N8: 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
GN SEPTUM SITE-DETERMINING PROTEIN MIND.  
OS Vibriol. cholerae.  
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
NCBI\_TaxID=666;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=EL TOR N16961 / SEROTYPE O1;  
RX MEDLINE=20406833; PubMed=10952301;  
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,  
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
RA Fraser C.M.;  
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
RT cholerae";  
RT Nature 406:477-483(2000).  
RL EMBL: AE004271; AAF95108.1; -;  
DR TIGR: VCI1960; -;  
DR InterPro: IPR000707; Para.  
DR Pfam: PF00991; Para; 1.  
KW Complete proteome.  
SQ SEQUENCE 276 AA; 30098 MW; 46CB44013A847E59 CRC64;

Query Match 28.3%; Score 468; DB 2: Length 276;  
Best Local Similarity 40.4%; Pred. No. 5.2e-28;  
Matches 112; Conservative 57; Mismatches 90; Indels 18; Gaps 7;

QY 59 RIVVITSGKGVGKTTTANVGLSLARIGFVVAIDADGLRNLDDLGLERNVANTCEV 118  
DB 9 RIVVITSGKGVGKTTTANVGLSLARIGFVVAIDADGLRNLDDLGLERNVANTCEV 68  
QY 119 VINGDCRLDALVRDGRKWSNFELLICISPRSKLPMFGGKALEMLVDALKTREGSPDFT 178  
DB 69 VINGEATLNLQALIKDRKNEMFLTPASOTRDKALTLTKDG--VORVLDLTK---EMGPDFI 123  
QY 179 IIDCPAGIDAGFTTATPANEAVALVTPDITLALRDADRVGLLECDGIR-----DIK-- 230  
DB 124 ICDSPAGIEGALMALYFADEAVITVTPPEVSVYSDRILGILQSKRAOGAPIKOH 183  
QY 231 MIVNVRVTDMIKGEDMMSVLDVQEMGLSLGLVLPEDSEVIRSTRNGRPFVLNKPPTLAG 290  
DB 184 LILTRVNPAPAVTQGMELSVQDVEIHLVPLIGVIPSQAVLNASNKGVPVTFDDQSD-AG 242

QY 291 LAFEQAMRLV-EQDSKAMVVEEPKRGFFSGG 326  
DB 243 QAVQDTVARLHGEQVEFRFL---TEAKKGLFKHLFGG 276

RESULT 13  
Q9JOY6 PRELIMINARY; PRT; 271 AA.  
AC Q9JOY6: 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
GN SEPTUM SITE-DETERMINING PROTEIN (SEPTUM SITE-DETERMINING PROTEIN MIND).  
OS Neisseria meningitidis (serogroup A), and  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
NCBI\_TaxID=65699; 491;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;  
RX MEDLINE=20222556; PubMed=10761919;  
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
RA Davies R.M., Davis P., Deavin K., Felwell T., Hamlin N., Holroyd S.,  
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,  
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
RA Whitehead S., Spratt B.G., Barrell B.G.,  
RT "Complete DNA sequence of a serogroup A strain of Neisseria  
RT meningitidis Z2491";  
RT Nature 404:502-506(2000).  
RN 12  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / SEROGROUP B;  
RX MEDLINE=20175755; PubMed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,  
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,  
RA Cotton M.D., Utterback T.R., Khouli H., Qin H., Vamathevan J.,  
RA Gill J., Scarlato V., Masigiani V., Pizzo M., Grandi G., Sun L.,  
RA Smith H.O., Fraser C.M., Moxon E.R., Rappelli R., Venter J.C.;  
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain  
RT MC58";  
RT Science 287:1809-1815(2000).  
RL EMBL: AL162752; CAB83415.1; -;  
DR EMBL: AE002374; AAF40628.1; -;  
DR TIGR: NMB0171; -;  
DR InterPro: IPR000707; Para.  
DR Pfam: PF00991; Para; 1.  
KW Complete proteome.  
SQ SEQUENCE 271 AA; 29559 MW; 9ACDB52A03BD6170 CRC64;

Query Match 27.2%; Score 449.5; DB 2: Length 271;  
Best Local Similarity 37.5%; Pred. No. 1.3e-26;  
Matches 104; Conservative 63; Mismatches 93; Indels 17; Gaps 7;

QY 59 RIVVITSGKGVGKTTTANVGLSLARIGFVVAIDADGLRNLDDLGLERNVANTCEV 118  
DB 3 RIVVITSGKGVGKTTTANVGLSLARIGFVVAIDADGLRNLDDLGLERNVANTCEV 62  
QY 119 VINGDCRLDALVRDGRKWSNFELLICISPRSKLPMFGGKALEMLVDALKTREGSPDFT 178  
DB 63 VINGEATLNLQALIKDRKNEMFLTPASOTRDKALTLTKDG--VORVLDLTK---EMGPDFI 123  
QY 179 IIDCPAGIDAGFTTATPANEAVALVTPDITLALRDADRVGLLECDGIR-----ECGDIRDKM 231  
DB 120 ICDSPAGIEGALMALYFADEAVITVTPPEVSVYSDRILGILQSKRAOGAPIKOH 183  
QY 231 MIVNVRVTDMIKGEDMMSVLDVQEMGLSLGLVLPEDSEVIRSTRNGRPFVLNKPPTLAG 290  
DB 184 LILTRVNPAPAVTQGMELSVQDVEIHLVPLIGVIPSQAVLNASNKGVPVTFDDQSD-AG 242

Db 180 LITRSPERVAKGEMLSVQDIDICDILHPLLGVPESQNVLAQNSGEP-VIHQDSVAASE 238  
 QY 292 AFEQAMRLV-EQDSMKAVMEEPKRGFFS-FEGG 326  
 Db 239 AYKDVIALRLGENRMRFL---EAEKKSFFKRLFGG 271

## RESULT 14

Q9AG19 PRELIMINARY: PRT: 271 AA.

AC Q9AG19: 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE MIND.  
 GN MIND.  
 OS *Neisseria gonorrhoeae*.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=485;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CH811;  
 RX MEDLINE=21097259; PubMed=11160816;  
 RA Ramirez-Arcos S., Szeto J., Beveridge T., Victor C., Francis F.,  
 RA Dillon J.;  
 RT "deletion of the cell-division inhibitor Minc results in lysis of  
 RT *Neisseria gonorrhoeae*."  
 RL Microbiology 147:225-237(2001).  
 DR EMBL: AF345908; AAK30126.1; -.  
 SQ SEQUENCE 271 AA; 29597 MW; 87EC6FE31067B542 CRC64;

Query Match 27.2%; Score 449.5; DB 2; Length 271;  
 Best Local Similarity 37.5%; Pred. No. 1.3e-26;  
 Matches 104; Conservative 63; Mismatches 93; Indels 17; Gaps 7;

QY 59 RIVVITSGKGVGKTTTANGLSLARYGSVAIDADLGLRNLDLLGLENRVNTCVE 118  
 Db 3 KIIIVTSGKGVGKTTTANGLSLARYGSVAIDADLGLRNLDLLGLENRVNTCVE 118  
 QY 119 VINGCDRLDQALVRDKRNSFELLCSKPRSKLPMFGKALEMLVDALKTREGSPDFI 178  
 Db 63 VIQGATLNGALIKKNCENLFLPASQTRDADLTREG--VEKVMQELSGKKMGF-EYI 119  
 QY 179 IIDCPAGIDAGFTTATPANEAVALTPDITALLRADRVYGLL-----ECGIRDIM 231  
 Db 120 ICDSFAGIEOGALMALYFADEAIVTNPVSSVRSDRIIGLQSKSRKAQOGGSVKEHL 179  
 QY 232 IVNRVTMIKGEDMMSVLDVQEMGLSLGVIPEDSEVIRSTNRFPLVLRKPTLAGL 291  
 Db 180 LITRSPERVAKGEMLSVQDIDICDILHPLLGVPESQNVLAQNSGEP-VIHQDSVAASE 238  
 QY 292 AFEQAMRLV-EQDSMKAVMEEPKRGFFS-FEGG 326  
 Db 239 AYKDVIALRLGENRMRFL---EAEKKSFFKRLFGG 271

## RESULT 15

Q9V165 PRELIMINARY: PRT: 260 AA.

AC Q9V165: 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE CELL DIVISION INHIBITOR (MIND-1).  
 GN PAB1983.  
 OS *Pyrococcus abyssi*.  
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.  
 OX NCBI\_TaxID=29292;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ORSAY;

RA Hellig R.;  
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome  
 RT structure and evolution."  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ248284; CAB49485.1; -.  
 DR InterPro: IPR000392; NitrogenaseII.  
 DR InterPro: IPR000707; ParaA.  
 DR Pfam: PF00142; fer4\_NIFH; 1.  
 DR Pfam: PF00991; Para; 1.  
 KW Cell division; Complete proteome.

QY SEQUENCE 260 AA; 27657 MW; 8C02C95C720A35B8 CRC64;

Query Match 22.1%; Score 366; DB 1; Length 260;  
 Best Local Similarity 32.9%; Pred. No. 2.9e-20;  
 Matches 94; Conservative 54; Mismatches 88; Indels 50; Gaps 7;

QY 59 RIVVITSGKGVGKTTTANGLSLARYGSVAIDADLGLRNLDLLGLENRVNTCVE 118  
 Db 4 RSIYFASGKGVGKTTTANGLSLARYGSVAIDADLGLRNLDLLGLENRVNTCVE 118  
 QY 119 VINGCDRLDQALVRDKRNSFELLCSKPRSKLPMFGF-----GKALEMLVDALKTREGSPDFI 173  
 Db 63 VINGCDRLDQALVRDKRNSFELLCSKPRSKLPMFGF-----GKALEMLVDALKTREGSPDFI 173  
 QY 174 -----SPDFIIDCPAGIDAGFTTATPANEAVALTPDITALLRADRVYGLLCEGDIR 227  
 Db 105 IREISQMGDFLIDAPAGLELITALLIGKELIIVTNPETALIDSLETKVAKELGTL 164  
 QY 228 DIKMIIVNRVTDMIKGEDMMSVLDVQEMGLSLGVIPEDSEVIRSTNRFPLVLRKPT 287  
 Db 165 PLGAILNRVTSEKTE---LSREIEALLEVPLTGVPEDEPKRASAGVPLVVKNPPTS 220  
 QY 288 LAGLAPEQAA-----WRLVEQDSMKAVMEEPKRGFFS-FEGG 326  
 Db 221 PAATAYKEIAKLAGIKKKPPEPS-----PVKRIFRALFGG 257

Search completed: February 11, 2002, 13:32:41  
 Job time: 88 sec







PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134370.  
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PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
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PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
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PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
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PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
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PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
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PR 25-OCT-1999; 99US-0161406.  
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DB 18 maslrflstnhgsllpsslsqktlissprvnnpsrrsrsrslqfrkrelgeprri 77  
QY 61 VVITSGKGVGKTTTNNAGSLARGFSSVAIDADGLRLDLLGLENVNTCYEVI 120  
DB 78 vvitsgkgvgktttntnagslargfssvaiddadgllnldllglenvntcyevi 137  
QY 121 NGDCRLDQALVRDKRMSNFELLCSKPRSKLPMGFGSKALEMVLDAKTRPGSPDFIII 180  
DB 138 ngdcrlidqalvrdrkmsnfellcskprsklpmgfgskalemlvdalktrpesspdfiii 197  
QY 181 DCPAGIDAGFTTATTPANENVLTTPDTITLRDADRTGGLCEGIRPKMIVNRVRDM 240  
DB 198 dcpagidagftalttpaneenvlttptaltlrdadrtvgllceqiridkmlvnrvtldm 257  
QY 241 IKGEDMMSVLDVOEMLSLILGVPEDSEVIRSTRNGFPVLNRPPLTAGLAFQAAWRL 300  
DB 258 ikgedmmsvldvomegslilgvpedsevirstrngfplvlnrppltaglafqaaawl 317  
QY 301 VEDDSKAAVVEEPKRRGFFSFFGG 326  
DB 318 vegdsakvamveepkrrgffsffgg 343

RESULT 3  
AAAG12922  
ID AAAG12922 standard; Protein: 326 AA.  
XX  
AC AAAG12922;  
XX  
DT 17-OCT-2000 (first entry)  
XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 12222.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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| XX | 25-FEB-1999; | 99US-0121825. |
| PR | 05-MAR-1999; | 99US-0123180. |
| PR | 09-MAR-1999; | 99US-0123548. |
| PR | 22-MAR-1999; | 99US-0123788. |
| PR | 23-MAR-1999; | 99US-0126264. |
| PR | 29-MAR-1999; | 99US-0126785. |
| PR | 01-APR-1999; | 99US-0127462. |
| PR | 06-APR-1999; | 99US-0128234. |
| PR | 08-APR-1999; | 99US-0128714. |
| PR | 16-APR-1999; | 99US-0129845. |
| PR | 19-APR-1999; | 99US-0130077. |
| PR | 21-APR-1999; | 99US-0130449. |
| PR | 22-APR-1999; | 99US-0130510. |
| PR | 23-APR-1999; | 99US-0130891. |
| PR | 28-APR-1999; | 99US-0131449. |
| PR | 30-APR-1999; | 99US-0132048. |
| PR | 30-APR-1999; | 99US-0132407. |
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| PR | 05-MAY-1999; | 99US-0132485. |
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| PR | 07-MAY-1999; | 99US-0132487. |
| PR | 11-MAY-1999; | 99US-0132863. |
| PR | 14-MAY-1999; | 99US-0134256. |
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| PR | 14-MAY-1999; | 99US-0134321. |
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| PR | 18-MAY-1999; | 99US-0134768. |
| PR | 19-MAY-1999; | 99US-0134941. |
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| PR | 21-MAY-1999; | 99US-0135253. |
| PR | 24-MAY-1999; | 99US-0135629. |
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| PR | 27-MAY-1999; | 99US-0136392. |
| PR | 28-MAY-1999; | 99US-0136782. |
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| PR | 03-JUN-1999; | 99US-0137528. |
| PR | 04-JUN-1999; | 99US-0137502. |
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| PR | 08-JUN-1999; | 99US-0138060. |
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| PR | 14-JUN-1999; | 99US-0139119. |
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| PR | 17-JUN-1999; | 99US-0139492. |
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| PR | 18-JUN-1999; | 99US-0139462. |
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| PR | 24-JUN-1999; | 99US-0140695. |
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| PR | 06-JUL-1999; | 99US-0142390. |
| PR | 08-JUL-1999; | 99US-0142803. |
| PR | 09-JUL-1999; | 99US-0142920. |
| PR | 12-JUL-1999; | 99US-0142977. |
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| PR | 22-JUL-1999; | 99US-0145085. |
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| PR | 18-AUG-1999; | 99US-0149175. |
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| PR | 23-AUG-1999; | 99US-0149930. |
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Query Match 99.68; Score 1648; DB 21; Length 326;  
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 QY 61 VITSGKGVKTTTAVGSLARVGFVVAIDADLGRINDLLGLENNRVNVCVEVT 120  
 DB 61 vitsgkgvktttavngslarvgsfvaiddadlgrindlllglenrvnvcvevt 120  
 QY 121 NGDCRLDQALVRDRKWSNFELLCISKPRSKLPMGFGKALEWLVALKTRPGSPDFIT 180  
 DB 121 ngdcrlldqalvrdrkwsnfellicskprsklpmgfgkalewlvalktrpgspdfit 180  
 QY 181 DCPAGIAGFTTATTPANEAVLTPPTOTALDADRVTVGLLECDSDIRIKMIVNRYRDM 240  
 DB 181 dcpaglagfttattpaneavltppdtalrdadrvtvglllecddiridkmiinvrtdm 240  
 QY 241 IKGEDMMSVLDVOMIGSLIGVTPEDSEVTRSTNRGFPVYNKRPPTLAGLAFEDAAWRL 300  
 DB 241 ikgedmmsvldvomigsligvtpedsevtstnrgfpvynkrrpptlaglafedaaawl 300

QY 301 VEODSMKAVVEEPPKKRGFFSEFEGG 326  
 DB 301 veodsmkavmveeppkkrgffsffgg 326  
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 XX  
 DT 17-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 12221.  
 XX  
 KW Protein identification: signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN EP1033405-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 25-FEB-2000; 2000EP-0301439.  
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 PR 05-MAR-1999; 99US-0123180.  
 PR 09-MAR-1999; 99US-0123548.  
 PR 23-MAR-1999; 99US-0125788.  
 PR 25-MAR-1999; 99US-0126264.  
 PR 29-MAR-1999; 99US-0126785.  
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 PR 08-APR-1999; 99US-0128714.  
 PR 16-APR-1999; 99US-0129845.  
 PR 19-APR-1999; 99US-0130077.  
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 PR 23-APR-1999; 99US-0130510.  
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 PR 30-APR-1999; 99US-0132048.  
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 PR 04-MAY-1999; 99US-0132484.  
 PR 05-MAY-1999; 99US-0132485.  
 PR 06-MAY-1999; 99US-0132486.  
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Helicobacter pylori.

MO9818323-A1.

07-MAY-1998.

28-OCT-1997; 97WO-US19575.

14-JUL-1997; 97US-0891928.

28-OCT-1996; 96US-0739150.

06-DEC-1996; 96US-0759739.

(ASTRA ) ASTRA AB.

Alm RA, Smith D;

WPI: 1998-271811/24.

N-PSDB: AAX30457.

Helicobacter pylori nucleic acids and proteins - used to develop

products for the detection, prevention and treatment of H. pylori

infections

Claims 27, 31; Page 195; 279pp; English.

Recombinant or substantially pure preparations of H. pylori polypeptides

are disclosed, together with the nucleic acids encoding them. In all,

73 ORFs are shown. The proteins are variously cell envelope proteins,

secreted proteins or other cellular proteins. Vaccines containing at least

8 nucleotides from the nucleic acid sequences. The vaccines are useful

for treating or reducing the risk of H. pylori infections, and the

probes can be used diagnostically for detecting the presence of

Helicobacter in a sample. The products are also of use in screening

Query Match 13.5%; Score 224; DB 19; Length 294;

Best Local Similarity 29.1%; Pred. No. 4.4e-16;

Matches 87; Conservative 40; Mismatches 106; Indels 66; Gaps 11;

OY 55 GEPRIIVITSGKGVGTGTTTANVGLSLARYGFSVAVIDADLGRNLDLGLLENRVY 114  
Db 25 gnt-kfaietsgkgyvgsksanlsanlslaylkykyvgyvfdadiglanldvlgvntkn- 82  
OY 115 TCVEVINGDCRLDQALVRKMSNFELICISPKRSLPMG-----FGKALEMLV 164  
Db 83 -llhalkgeaklg-----elicelepgjcllpgdsgeelkylsgaealdrfv 129  
OY 165 DALKTRPEG---SPDFIITDCPAGIDAGTITATPANEAVALVTPDITALLRADAVTGLL 221  
Db 130 d-----eevylssldyivldtgagltgafinasdevvltvcpasaltca-----y 178  
OY 222 ECDGIR-----DINKIVNRV-----RTDMIKGEMMSVLDVOMLGLSLGVIP 265  
Db 179 acikinsknkdelfliamvqpkgralyerlfkvaknnlas-----lelhylgate 231  
OY 266 EDSEVIRSTNGEFLVLNKPPTLAGLAFEOAMRLVEDOSMKAVNVEEPPKRGFFSFP 324  
Db 232 nssllkryvrerkllrkiaipndllfsqidsqasllvskletgltl-----eipkeglskf 286

# RESULT 8

AAW20738  
ID AAW20738 standard; Protein: 297 AA.

AAW20738:

16-JUL-1997 (first entry)

H. pylori cytoplasmic protein, 06cp20302orf8.

Cytoplasmic; vaccine; prevention; treatment; infection; identification;

binding compound; bacterium; life cycle; activator; bacteria; inhibitor;

duodenal ulcer disease; chronic gastritis; diagnosis; envelope.

Helicobacter pylori.

MO9640893-A1.

19-DEC-1996.

06-JUN-1996; 96WO-US09122.

01-APR-1996; 96US-0630405.

07-JUN-1995; 95US-0487032.

(ASTRA ) ASTRA AB.

Berglindh OT, Smith D, Mellgaerd BL;

WPI: 1997-052306/05.

N-PSDB: AAT67991.

Helicobacter pylori nucleic acid sequences and related

polypeptide(s) - useful for vaccines to treat or prevent H. pylori

infection, and to detect Helicobacter

infection.

Claim 61; Page 1154; 1481pp; English.

The present sequence is a Helicobacter pylori cytoplasmic protein.

The protein may be used in a vaccine to prevent or treat H. pylori

infection or to identify H. pylori polypeptide binding compounds,

useful as potential H. pylori life cycle activators or inhibitors.

CC The present sequence is a Helicobacter pylori cytoplasmic protein.  
CC The protein may be used in a vaccine to prevent or treat H. pylori

PI Burr TJ, Herlache TC, Zhang H,  
XX

DR WPI; 2000-376567/32.  
DR N-PSDB; AAA61510.  
XX New protein from *Agrobacterium vitis*, useful e.g. for imparting  
PT resistance to disease or stress to plants, is involved in production of  
PT a hypersensitive response  
PS Claim 3; Page 112-113; 157pp; English.  
XX  
XX Sequences AAB1630-B1688 represent proteins from *Agrobacterium vitis*  
CC which elicit a hypersensitivity response (HR) in a plant. The invention  
CC also relates to nucleotide sequences (AAA61501-A61524) encoding the A.  
CC vitis HR elicitor proteins. The HR is a rapid, localised necrosis that  
CC is associated with the active defence of plants against many pathogens,  
CC and occurs when a pathogenic organism interacts with a nonhost plant.  
CC (i.e. one in which intracellular bacterial growth and disease development  
CC do not occur). Like other HR elicitors, the A. vitis elicitor functions  
CC in non-host plants by causing a rapid hypersensitive response that  
CC results in walling-off and killing of the pathogen. On grape plants, the  
CC A. vitis elicitor induces a restricted necrosis of tissues, resulting in  
CC the death of plant cells and induction of pathogen resistance. A. vitis  
CC HR elicitor proteins, in non-infectious form, are used to treat plants or  
CC their seeds to impart resistance to disease, such as those caused by  
CC fungi, bacteria or viruses; and to enhance growth, e.g., to increase  
CC yield or to provide earlier germination or maturation. The proteins can  
CC also be used to control insects, to impart resistance to environmental  
CC stresses, e.g., cold, and to improve nutritional value, e.g., altered oil  
CC content. The same effects can be produced by producing transgenic plants  
CC or seeds by incorporation of DNA that encodes A. vitis HR elicitor  
CC proteins. Use of A. vitis HR elicitor proteins, or nucleic acids encoding  
CC them, may allow control of previously untreatable diseases; provide  
CC systemic treatment; and eliminate the need for biological control agents  
CC or polluting chemicals.  
XX  
XX Sequence 388 AA:  
SQ  
Query Match 12.5%; Score 206; DB 21; Length 388;  
Best Local Similarity 25.9%; Pred. No. 6.7e-14;  
Matches 72; Conservative 48; Mismatches 100; Indels 58; Gaps 10;  
QY 60 IVVITSGGKGVKTTTANVGLSLARYGSVAIDDLRLNLDLLENNRYNYTCVEV 119  
DB 131 IIVASGKGYGKSTAVLALALLANGILKVGILDDAVYGPSMPRLIGISRPQ----- 184  
QY 120 INDCRLQALVRDRKWSNFELLCISKPSKLPWCF---GKALEW-----LVDAK 168  
DB 185 -----qldgrll-vpmenygikams-----igflvdegatamiwrgpvmgsalmgmrlr 230  
QY 169 TRPESPEIITDCPAGIDAGFITAT--TPANAVLVTPPDITALLRDAKVTGLLECDGI 226  
DB 231 evaweladlvavdmpgtdaqclmaqyvlsgavlvscpdaialldatrgimffkvev 290  
QY 227 RDKIMIVNR-----VRTMI-----KGEDMSVLVDQENLGLSLGVIPEDSEVIR 272  
DB 291 pvlgylemysfiapdtgrtydflfnggaka-----aealgapflfpltsire 342  
QY 273 STNNGEPPLVLPKPTLAGLAFEQAA---WRLVEODSMK 307  
DB 343 hsdagtlpvvseepspqalvyreialtrwreverhstr 380  
RESULT 11  
ID AAM20443  
ID AAM20443 standard; protein; 412 AA.  
XX  
XX AAM20443;  
AC  
XX 14-JUL-1997 (first entry)  
DT  
XX H. pylori cytoplasmic protein, 35163962.aa.  
DE  
XX Cytoplasmic; vaccine; prevention; treatment; infection; identification;  
KW

KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;  
KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.  
XX  
XX Helicobacter pylori.  
XX  
XX W09640893-A1.  
XX  
XX 19-DEC-1996.  
XX  
XX 06-JUN-1996; 96W0-US09122.  
XX  
XX 01-APR-1996; 96US-0630405.  
XX  
XX 07-JUN-1995; 95US-0487032.  
XX  
XX (ASTR ) ASTRA AB.  
XX  
XX Berglindh OT, Smith D, Møllgaard BL;  
XX  
XX WPI; 1997-052306/05.  
XX N-PSDB; AAT67616.  
XX  
XX Claim 61; Page 617-618; 1481pp; English.  
XX  
XX The present sequence is a Helicobacter pylori cytoplasmic protein.  
CC The protein may be used in a vaccine to prevent or treat H. pylori  
CC infection or to identify H. pylori polypeptide binding compounds, useful  
CC as potential H. pylori life cycle activators or inhibitors. The genomic  
CC sequence of H. pylori (ATCC 55679) was determined from overlapping  
CC contigs generated by mechanically shearing the bacterial DNA. The  
CC sequences were analysed for ORF of at least 180 nucleotides, and the  
CC predicted coding regions defined by computer evaluation. To identify  
CC likely H. pylori antigens for vaccine development, the amino acid  
CC sequences predicted from various ORF were analysed for significant  
CC homology to other known or exported membrane proteins. Having identified  
CC and determined the sequences of interest, particular regions can be  
CC isolated from H. pylori by PCR amplification for recombinant polypeptide  
CC production, e.g. in E. coli hosts.  
XX  
XX Sequence 412 AA:  
SQ  
Query Match 12.0%; Score 198; DB 18; Length 412;  
Best Local Similarity 23.9%; Pred. No. 5.7e-13;  
Matches 79; Conservative 56; Mismatches 114; Indels 82; Gaps 12;  
QY 8 STNHSLLPSSLQKTLISSPRFVNNPSPRSIRSVLQFNKPE-----LAGETPR 59  
DB 92 sseetsallrenslkamgkykaldtkpp-----kpgqpkptcknlaknlkh 142  
QY 60 IVVITSGGKGVKTTTANVGLSLARYGSVAIDDLRLNLDLLENNRYNYTCVEV 119  
DB 143 vvmlassggygkstvnslalanlqkvgllldadvypnlprrmgilq----- 192  
QY 120 INDCRLQALVRDRKWSNFELLCISKPSKLPWCF---GKALEWLVDAKLTTRPE- 172  
DB 193 -nadvimpsgkklipkafg-----vsmsmglllydegqglivrgplmlraeq 241  
QY 173 -----GSPDFIITDCPAGID--AGFTTATPANAVLVTPPDITALLRDAK----- 216  
DB 242 mlsdliwgdldlvvdmprrncrcahaaavplsagltvctpqivslidakxslmfxk 301  
QY 217 -----WTGILE-----CDGIRDKIMIVNRVRTMIGEDMSVLVDQENLGLSLGVIPED 266  
DB 302 lhiplagivemsgstvcenck-----keselfgmsmgll--leayngtlaklpl 350  
QY 267 DSEVIRSTNNGEPPLVLPKPTLAGLAFEQAA 297  
DB 351 epkvrlygdgkgeplivshpstsaklfekma 381

RESULT 12  
AAG93171  
ID AAG93171 standard; Protein; 279 AA.  
XX  
AC AAG93171;  
XX  
DT 26-SEP-2001 (first entry)  
XX  
DE C glutamicum protein fragment SEQ ID NO: 6925.  
XX  
KM Corynebacterium; amino acid synthesis; vitamin; saccharide;  
XX organic acid synthesis.  
XX  
OS Corynebacterium glutamicum.  
XX  
PN EPI108790-A2.  
XX  
PD 20-JUN-2001.  
XX  
PF 18-DEC-2000; 2000EP-0127688.  
XX  
PR 16-DEC-1999; 99JP-0377484.  
XX 07-APR-2000; 2000JP-0159162.  
XX 03-AUG-2000; 2000JP-0280988.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
PI Tateishi N, Senoh A, Ikeda M, Ozaki A,  
XX  
DR WPI: 2001-376931/40.  
XX N-PSDB: AAH68390.  
XX  
PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying  
PT mutation point of a gene, measuring expression of a gene, analysing  
PT expression profile or pattern of a gene and identifying homologous gene  
PT  
XX  
XX Claim 17; SEQ ID NO: 6925; 246bp + Sequence Listing; English.  
XX  
XX The present invention provides a number of nucleotide and protein  
CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These  
CC are useful for identifying the mutation point of a gene derived from a  
CC mutant of corynebacterium bacterium, measuring expression amount and  
CC analysing the expression profile or expression pattern of a gene derived  
CC from Corynebacterium bacterium, and identifying a homologue of a gene derived  
CC from corynebacterium bacterium. Corynebacterium bacteria are useful for producing  
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,  
CC particularly L-lysine. The present sequence is a protein described  
CC in the exemplification of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC European Patent Office.  
XX  
XX Sequence 279 AA;  
SQ  
Query Match 11.9%; Score 197.5; DB 22; Length 279;  
Best Local Similarity 26.4%; Pred. No. 3.5e-13;  
Matches 71; Conservative 46; Mismatches 109; Indels 43; Gaps 10;  
XX  
OY 58 PRIVVITSGKGVKTTTANVAVGLSARYSVVAIDADLGRINDLLIGENRV-NWTC 116  
DB 7 p r i l l a n g k y g y g k t t s t v l a a s l a i h g l k v l v d i d - p g n a s t a l g y h r s g t l s 65  
OY 117 VEVINGDCRDLQALVRKRMGNFELCTSKPRSKLPMGFGALWM-----LVNVL 167  
DB 66 y e l l i g e c t a d e a m - q p s t a n e m f c l - - - - - p a t i l a g a e l v s l v r r e y r l a d a l 118  
OY 168 KTR-PEGSDPFIIDCPAGIDAGTATTPANEAVLVTTPDITLRADRVYGLLECDG 225  
DB 119 g r e f i d k h d f d y m l d c p p s i g l l t i n a m t a v n e v l i p d i c e y a l e g y g d - - - - - l n n 173

OY 226 IRDVKMIVNR-----VRTDMIKGDDMSVLDVQEMLGSLIG-VIPEDSEVI 271  
DB 174 l t m l r g h n r q l h s a i l l t m y d a r t n l a e - - - - - q v a t e v n d h f g d v l g n k h i p r s v k v s 229  
OY 272 RSTNRGPEPLVINKPEPTLAGLAFEQAAMRL 300  
DB 230 e a p y g g t v l e y d p g s r g a m a y l d a a k e l 258  
RESULT 13  
AAG81141  
ID AAG81141 standard; Protein; 390 AA.  
XX  
AC AAG81141;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Mycobacterium tuberculosis potential drug target protein SEQ ID 192.  
XX  
KM Drug target; growth; organism viability; characterisation.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN WC200135317-A1.  
XX  
PD 17-MAY-2001.  
XX  
PF 13-NOV-2000; 2000WO-US31152.  
XX  
PR 12-NOV-1999; 99US-0165086.  
XX 12-NOV-1999; 99US-0165124.  
XX 01-FEB-2000; 2000US-0179531.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Eisenberg D, Rotstein SH, Marcotte EM;  
XX  
DR WPI: 2001-329193/34.  
XX N-PSDB: AAH51992.  
XX  
PT Identifying nucleotide or polypeptide sequence for use as drug target,  
PT involves providing algorithm that analyzes a functional relationship  
PT between nucleotide or polypeptide sequences, and comparing the  
PT sequences  
XX  
XX Disclosure; Page 166; 207pp; English.  
XX  
XX This invention relates to a method for identifying a nucleotide or  
CC polypeptide sequence that may be a drug target, or essential for growth  
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092  
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium  
CC tuberculosis proteins which are potential drug targets. The DNA and  
CC protein sequences are used to illustrate the method of the invention. The  
CC method involves providing an unknown nucleotide or polypeptide sequences,  
CC and comparing it to a number of sequences along with at least one  
CC algorithm capable of analysing a functional relationship between  
CC nucleotide and polypeptide sequences. The method is useful for  
CC characterising the function of nucleic acids and polypeptides that may be  
CC useful as a target for a drug or essential for the growth or viability of  
CC an organism.  
XX  
XX Sequence 390 AA;  
SQ  
Query Match 11.5%; Score 190; DB 22; Length 390;  
Best Local Similarity 24.0%; Pred. No. 4e-12;  
Matches 68; Conservative 58; Mismatches 117; Indels 40; Gaps 9;  
OY 32 VNNPSRRSPRISVLOFN-RKPELAGETP---RVVITSGKGVKTTTANVAVGLSARY 86  
DB 95 v n s d e q r t e l r k q l r d t r e p v i p f a q p d s l t r v a v a s k g y g k s t v n l a a m a v r 154



| Query Match           | 11.1%  | Score 183  | DB 21     | Length 313 |
|-----------------------|--|--|-----------|------------|
| Best Local Similarity | 22.9%  | Pred. 1.7e-11  |           |            |
| Matches 64            | Conservative 54  | Mismatches 88  | Indels 74 | Gaps 12    |
| QY                    | 60   | IVVITSGKGVCKTTTNAVGLSLA-RYGFSSVALDADGLNLDLLGLENRVNTCYE     | 118       |            |
| DB                    | 45   | IIIVASGKGVKGVKSTAVLAVALKCEIKIGLIDADVGSVPVIMNINIKPKV----    | 99        |            |
| QY                    | 119  | VINGDCRLDQALVRDKRMSNFELCTISK--PRSKLPMGFGC-----KALEMLV      | 164       |            |
| DB                    | 100  | -VNGDKMKMPV-----ENYGVKCMNSGIIIVKQAPLWIRGPMWSALAKMTKYDV--   | 149       |            |
| QY                    | 165  | DALKTRPESPPFIILDCPAGI-DAGF-ITAITPANEAVLVYTPITLALRDADR----- | 216       |            |
| DB                    | 150  | -----GDLIDLVDMPPGTGDAQISISQNLKISGAVISTPQDVALADNRGISMFD     | 201       |            |
| QY                    | 217  | -----VTGLE-----CGIRDIMIVNRV--RTDMIKGEDMMSVLDVOCMLGSLTG     | 262       |            |
| DB                    | 202  | KYRVPILGLIVENMSCFVCPHCNEPSFIIFGKEGARTAAK-----GKIIIG        | 247       |            |
| QY                    | 263  | VIPDESEVIRSTNRGEPPLVLPKPPPLAGIAFEQAAMRLVE                  | 302       |            |
| DB                    | 248  | EIPLEMSIREGSDGVYVVSSEPSGIVSKAYGLAGNVAK                     | 287       |            |
| RESULT 15             |  |  |           |            |
| AA643414              |  |  |           |            |
| ID                    | AA643414   | standard; Protein: 313 AA.                                 |           |            |
| XX                    | AA643414   |  |           |            |
| AC                    | AA643414   |  |           |            |
| XX                    | AA643414   |  |           |            |
| DT                    | 18-OCT-2000  | (first entry)  |           |            |
| XX                    | AA643414   |  |           |            |
| DE                    | Arabidopsis thaliana protein fragment SEQ ID NO: 54260.  |  |           |            |
| XX                    | AA643414   |  |           |            |
| KW                    | Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence. |  |           |            |
| OS                    | Arabidopsis thaliana.  |  |           |            |
| XX                    | AA643414   |  |           |            |
| PM                    | EP1033405-A2.  |  |           |            |
| XX                    | AA643414   |  |           |            |
| PD                    | 06-SEP-2000.   |  |           |            |
| XX                    | AA643414   |  |           |            |
| PF                    | 25-FEB-2000; 2000EP-0301439.   |  |           |            |
| XX                    | AA643414   |  |           |            |
| PR                    | 25-FEB-1999;   | 99US-0121825;  |           |            |
| PR                    | 05-MAR-1999;   | 99US-0123180;  |           |            |
| PR                    | 09-MAR-1999;   | 99US-0123548;  |           |            |
| PR                    | 23-MAR-1999;   | 99US-0125788;  |           |            |
| PR                    | 25-MAR-1999;   | 99US-0126264;  |           |            |
| PR                    | 29-MAR-1999;   | 99US-0126785;  |           |            |
| PR                    | 01-APR-1999;   | 99US-0127462;  |           |            |
| PR                    | 06-APR-1999;   | 99US-0128234;  |           |            |
| PR                    | 08-APR-1999;   | 99US-0128714;  |           |            |
| PR                    | 16-APR-1999;   | 99US-0129845;  |           |            |
| PR                    | 19-APR-1999;   | 99US-0130077;  |           |            |
| PR                    | 21-APR-1999;   | 99US-0130449;  |           |            |
| PR                    | 23-APR-1999;   | 99US-0130510;  |           |            |
| PR                    | 23-APR-1999;   | 99US-0130881;  |           |            |
| PR                    | 28-APR-1999;   | 99US-0131449;  |           |            |
| PR                    | 30-APR-1999;   | 99US-0132048;  |           |            |
| PR                    | 30-APR-1999;   | 99US-0132407;  |           |            |
| PR                    | 04-MAY-1999;   | 99US-0132484;  |           |            |
| PR                    | 05-MAY-1999;   | 99US-0132485;  |           |            |
| PR                    | 06-MAY-1999;   | 99US-0132486;  |           |            |
| PR                    | 06-MAY-1999;   | 99US-0132487;  |           |            |
| PR                    | 07-MAY-1999;   | 99US-0132863;  |           |            |
| PR                    | 11-MAY-1999;   | 99US-0134256;  |           |            |
| PR                    | 14-MAY-1999;   | 99US-0134218;  |           |            |
| PR                    | 14-MAY-1999;   | 99US-0134219;  |           |            |



PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139765.  
PR 18-JUN-1999; 99US-0139766.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140699.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143342.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145066.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147316.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 17-AUG-1999; 99US-0149368.  
PR 18-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 01-SEP-1999; 99US-0151430.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 16-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 23-OCT-1999; 99US-0161404.



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OM protein - protein search, using sw model

Run on: February 11, 2002, 13:31:13 ; Search time 12.59 Seconds  
(without alignments)  
582.690 Million cell updates/sec

Title: US-09-553-431-2

Perfect score: 1654  
Sequence: 1 MASLRLESTNHOSLLPSSL.....KAVWEDEPKKRGFFSFGG 326

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/CTOS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 88.5  | 5.4         | 264    | 3     | US-08-969-644-16   |
| 2          | 88.5  | 5.4         | 264    | 3     | US-08-444-189-16   |
| 3          | 88.5  | 5.4         | 264    | 3     | US-08-468-544-16   |
| 4          | 88.5  | 5.4         | 519    | 3     | US-08-997-445D-2   |
| 5          | 88    | 5.3         | 376    | 4     | US-09-461-474-6    |
| 6          | 88    | 5.3         | 732    | 5     | PCR-US95-17026-2   |
| 7          | 87    | 5.3         | 249    | 1     | US-08-597-236-5    |
| 8          | 87    | 5.3         | 249    | 1     | US-08-746-682A-5   |
| 9          | 86.5  | 5.2         | 416    | 3     | US-09-320-878-18   |
| 10         | 86.5  | 5.2         | 416    | 4     | US-09-105-537-39   |
| 11         | 85.5  | 5.2         | 1068   | 4     | US-09-085-1199B-11 |
| 12         | 83.5  | 5.0         | 3077   | 6     | 5223423-2          |
| 13         | 83.5  | 5.0         | 3457   | 2     | US-08-416-603-4    |
| 14         | 82.5  | 5.0         | 367    | 2     | US-08-896-320-1    |
| 15         | 82.5  | 5.0         | 367    | 2     | US-08-896-320-3    |
| 16         | 82.5  | 5.0         | 396    | 4     | US-09-461-474-2    |
| 17         | 82.5  | 5.0         | 756    | 4     | US-08-434-730-16   |
| 18         | 81.5  | 4.9         | 5087   | 4     | US-09-144-085-1    |
| 19         | 81    | 4.9         | 920    | 3     | US-08-930-996A-8   |
| 20         | 80.5  | 4.9         | 812    | 1     | US-08-446-794A-2   |
| 21         | 80.5  | 4.9         | 812    | 1     | US-08-750-007-3    |
| 22         | 80.5  | 4.9         | 812    | 2     | US-08-945-024-2    |
| 23         | 79    | 4.8         | 1041   | 1     | US-08-220-151-4    |
| 24         | 79    | 4.8         | 1041   | 1     | US-08-413-118-4    |
| 25         | 79    | 4.8         | 1041   | 3     | US-08-473-446-4    |
| 26         | 78.5  | 4.7         | 371    | 3     | US-08-837-593-8    |
| 27         | 78.5  | 4.7         | 676    | 4     | US-09-085-1199B-7  |

#### ALIGNMENTS

|    |      |     |      |   |                   |                    |
|----|------|-----|------|---|-------------------|--------------------|
| 28 | 78   | 4.7 | 332  | 4 | US-09-461-474-15  | Sequence 15, Appl  |
| 29 | 78   | 4.7 | 333  | 2 | US-08-674-149A-2  | Sequence 2, Appl1  |
| 30 | 78   | 4.7 | 937  | 1 | US-08-253-155A-31 | Sequence 31, Appl  |
| 31 | 78   | 4.7 | 3567 | 2 | US-07-642-734C-4  | Sequence 4, Appl1  |
| 32 | 78   | 4.7 | 3567 | 3 | US-08-439-009A-4  | Sequence 4, Appl1  |
| 33 | 77.5 | 4.7 | 325  | 4 | US-09-088-435-1   | Sequence 4, Appl1  |
| 34 | 77.5 | 4.7 | 2037 | 4 | US-09-306-938-3   | Sequence 1, Appl1  |
| 35 | 77   | 4.7 | 420  | 4 | US-09-066-047-8   | Sequence 8, Appl1  |
| 36 | 77   | 4.7 | 553  | 4 | US-09-413-814-3   | Sequence 3, Appl1  |
| 37 | 76   | 4.6 | 694  | 1 | US-08-164-839-4   | Sequence 4, Appl1  |
| 38 | 76   | 4.6 | 694  | 1 | US-08-583-799-4   | Sequence 4, Appl1  |
| 39 | 76   | 4.6 | 695  | 1 | US-08-164-839-6   | Sequence 6, Appl1  |
| 40 | 76   | 4.6 | 695  | 1 | US-08-583-799-6   | Sequence 6, Appl1  |
| 41 | 76   | 4.6 | 943  | 3 | US-08-911-321-4   | Sequence 4, Appl1  |
| 42 | 75.5 | 4.6 | 2616 | 6 | US-08-948-176-26  | Sequence 26, Appl1 |
| 43 | 75   | 4.5 | 371  | 2 | US-08-282-141-2   | Sequence 2, Appl1  |
| 44 | 75   | 4.5 | 678  | 1 | US-08-435-434-2   | Sequence 2, Appl1  |
| 45 | 75   | 4.5 | 678  | 1 | US-08-435-434-2   | Sequence 2, Appl1  |

RESULT 1  
US-08-969-644-16  
Sequence 16, Application US/08969644  
Patent No. 6096519  
GENERAL INFORMATION:  
APPLICANT: Ratti, Giulio  
APPLICANT: Comanducci, Maurizio  
APPLICANT: Tecce, Mario F.  
APPLICANT: Giuliani, Marzia M.  
TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA  
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY  
TITLE OF INVENTION: THEM: RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID  
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
STREET: 301 N. Washington Street  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22046-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/969,644  
FILING DATE: 13-NOV-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/467,152  
FILING DATE:  
APPLICATION NUMBER: US/07/661,820  
FILING DATE:  
APPLICATION NUMBER: IT MI 91A00314  
FILING DATE: 07-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 1677-202P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ. ID NO.: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 264 amino acids  
TYPE: amino acid  
TOPOLOGY: linear



SEQUENCE CHARACTERISTICS:  
LENGTH: 264 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-544-16

Query Match 5.4%: Score 88.5; DB 4; Length 264;  
Best Local Similarity 24.0%: Pred. No. 0.09; Indels 78; Gaps 7;

Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

QY 61 VVITSGKGVGKTTTANVGLSLARY-GFSVAIDADLGLRLDLLGLENRVNTVCVEV 119  
DB 4 LVFCSFGKGTGKTTLSLVGCGNLQFLGKKVLLADD-POSNLSGLG----- 50  
QY 120 INGCRLDQALVROKRWSNFEL--LCISKPRS--KLPMFGGKALEMLVDALKTRPES 174  
DB 51 --ASVRSQKGLHDVYTSNDLSKSTICETKDSVDLIPFSFSEQREL--DIHRGPSNN 106  
QY 175 -----PDFIITDCPAGIDAGFITATPANEAVALVTPDITLALRDADRVTGLE 222  
DB 107 LKLFNEYCAEFYDICIITDPISLGLTKFAFVAGDKLIACLTPPEFSILGQKIREPLS 166  
QY 223 CDG 225  
DB 167 SVG 169

RESULT 4  
US-08-997-445D-2  
Sequence 2, Application US/08997445D  
Patent No. 6043342  
GENERAL INFORMATION:  
APPLICANT: Kochev, Olivier N.  
TITLE OF INVENTION: PDZK1 Protein Containing PDZ  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David Prashker, Esq.  
STREET: P.O. Box 67  
CITY: Brookline  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02146  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 MB storage  
COMPUTER: IBM PS/1  
OPERATING SYSTEM: MS DOS  
SOFTWARE: WordPerfect version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/997,445D  
FILING DATE: December 23, 1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: David Prashker  
REGISTRATION NUMBER: 29,693  
REFERENCE/DOCKET NUMBER: BIS-037  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 232-7509  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 519 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-997-445D-2

Query Match 5.4%: Score 88.5; DB 3; Length 519;  
Best Local Similarity 19.3%: Pred. No. 0.27; Indels 107; Gaps 12;  
Matches 53; Conservative 38; Mismatches 76; Indels 107; Gaps 12;

QY 32 VNNPSRRSPIRSVLOFNRPK---ELAGETPRIVITSGKGVGKTTTANVGLSLARYGF 88  
DB 212 VDKETDKRHEOKIOFKREITASLKLPHQPIVEMKKGSNG-----YGF 255  
QY 89 SYVA-----IDA-----DLGLRLDLLGLENRVNTVCVEVINGDCRD----- 127  
DB 256 YLRAGEOKGCOIINKIDISGSPAEAGLKNNDLVVA---VNGESVETLDHDSVEMIRKG 311  
QY 128 ---QALVRKRWSNFELCISKP-----RSKLPMFGGKALEMLVDALKTRPESPDFI 178  
DB 312 GDQTSLLVVDKETNMVIRAFSPFLYQSOELPMG-----SVKEAPPTPSL 360  
QY 179 IIDCP-----AGIDAGFITATPANEAVALVTPDI 208  
DB 361 EVSSPPTTEEVDRPKLCRLAKGENGYFHLMAIRGLPGSFIRKVGKGA-----DL 414  
QY 209 TALRDADRVTGLEPCDDGIRDI---KMIYVNRVT 238  
DB 415 AGLEDEVI---IEVNGVNVLDPEYKVDRIQS 445

RESULT 5  
US-09-461-474-6  
Sequence 6, Application US/09461474  
Patent No. 6278042  
GENERAL INFORMATION:  
APPLICANT: Allen, Steve  
APPLICANT: Rafalski, Antoni  
APPLICANT: Sakai, Hajime  
TITLE OF INVENTION: Plant Metal Transporters  
FILE REFERENCE: BBI303 US NA  
CURRENT APPLICATION NUMBER: US/09/461,474  
EARLIER FILING DATE: 1999-12-14  
EARLIER APPLICATION NUMBER: 60/112,562  
EARLIER FILING DATE: 1998-12-16  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 6  
LENGTH: 376  
TYPE: PRT  
ORGANISM: Trilicium aestivum  
US-09-461-474-6

Query Match 5.3%: Score 88; DB 4; Length 376;  
Best Local Similarity 34.0%: Pred. No. 0.18; Indels 14; Gaps 5;  
Matches 33; Conservative 15; Mismatches 35;

QY 3 SLRLESTNHQSLLPSSLSQKTLISSPRVNNPSRRSPIRS---VLOFNRPKELAGETPR 59  
DB 12 SLILFS-RHQ-----LRORLT--QPHRTFRPKMSTAVISADMLPSLSLDDRSLR 61  
QY 60 IVVITSGKGVGKTTTANVGLSLARYGFSVAIDAD 96  
DB 62 WIFV-GKKGVGTITSSCSLAIQLAKVRRSVLLISTD 97

RESULT 6  
PCT-US95-17026-2  
Sequence 2, Application PC/TUS9517026  
GENERAL INFORMATION:  
APPLICANT: Zymogenetics, Inc.  
APPLICANT: 1201 Eastlake Avenue East  
APPLICANT: Seattle  
APPLICANT: WA  
APPLICANT: USA  
APPLICANT: 98102  
TITLE OF INVENTION: Bovine Factor XIII  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle

STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/17026  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31-648  
REFERENCE/DOCKET NUMBER: 94-18PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 732 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-17026-2

Query Match 5.3%; Score 88; DB 5; Length 732;  
Best Local Similarity 24.2%; Pred. No. 0.53;

Matches 72; Conservative 38; Mismatches 94; Indels 94; Gaps 20;

QY 34 NPSRRSPIRVLQFNKPE---LAGETPRIVITSGKGVGKTTTANGLST----- 83  
DB 255 NPIKSVRSVGSAM-IRAKDDEGVYAGSMQNVYAY-----GVPSAMTGSVDILLETSSQK 308  
QY 84 -ARGFSVALDADLGLNLDL-LGLENRV--NTCCEVINGDCRLD-----OA 129  
DB 309 PVRGQGCWVF---AGVNTFLRCIGIPARVVTNFSADNDNANQLDLEEDGNVNSK 364  
QY 130 LVPRDRMSNFELCTSK---PRSKLPMGFGKALEMLVDALKTREPGSPDFTIIDCPAGI 186  
DB 365 LTKDSVW-NYH--CMNEAMMRPDLPGVFGG---WQY--VISTFOENDGMTRCGPASY 415  
QY 187 -----DAGFITAITPANEAVLVTPDITALRDADRVGTGLEC----- 223  
DB 416 QAIKHGVCFQFADAPVFA--EVNSDLVY---VTAKKDGTHVEALDTTHIGKLIYTK 469  
QY 224 ---DGIDIKIIVRVRIDMK---GPDMSVLDOEMLG---LSLGVIPEDSEV 270  
DB 470 IGGDKMDI-----TDYKFOEGOEERLLETAMYGAKKALNTEGVLSKSDV 519

## RESULT 7

US-08-597-236-5  
Sequence 5, Application US/08597236  
Patent No. 573765  
GENERAL INFORMATION:  
APPLICANT: STINGELE, Francesca  
APPLICANT: MOLLET, Beat  
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americans  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/597,236  
FILING DATE:  
CLASSIFICATION: 426  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95201669.9  
FILING DATE: 20-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fanucci A., Allan  
REGISTRATION NUMBER: 30256  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-597-236-5

Query Match 5.3%; Score 87; DB 1; Length 249;  
Best Local Similarity 20.8%; Pred. No. 0.12;  
Matches 48; Conservative 40; Mismatches 79; Indels 64; Gaps 10;

QY 41 IRSVLOFNKPE-----LAGETPRIVITSGKGVGKTTTANVGLSLARYGES 89  
DB 7 VKSKVDPRAKTEEYNAIRNIQFSGAOMKVIAISSVAGSKSISVNLAISSVASIGR 66  
QY 90 VVALDADLGRNLDLGLLENRVYTCVEVINGDCRLDQALVRDKRMSNF-----EL 141  
DB 67 TLIDAE--TRN-----SVLSGTFKSNPEY---KGLSNFLSGNADLNET 105  
QY 142 LC---IS-----KPSKLPMGFGKALEMLVDALKTREPGSPDFTIIDC-PAG 185  
DB 106 ICOTDISGLDVYASGPVPNPTSLQ---NDNFRHMEVARS---CYDVIIIDTPVPG 157  
QY 186 IDAGFITAITPANEAVLVTPDITALRDADRVGTGLECDGIRDKIMYNRV 236  
DB 158 LVVIDAVIQAQDASLVTETAGIKRRFYTKAVQDLVSSGSQFLGVYLVNKV 208

## RESULT 8

US-08-746-682A-5  
Sequence 5, Application US/08746682A  
Patent No. 5766184  
GENERAL INFORMATION:  
APPLICANT: STINGELE, Francesca  
APPLICANT: MOLLET, Beat  
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americans  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/746,682A  
FILING DATE: 14-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/597,236  
FILING DATE: 20-JUN-1995  
APPLICATION NUMBER: EP 95201669.9  
FILING DATE: 20-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: FANUCCI A., Allan  
REGISTRATION NUMBER: 30256  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-746-682A-5

Query Match 5.3%; Score 87; DB 1; Length 249;  
Best Local Similarity 20.8%; Pred. No. 0.12;  
Matches 48; Conservative 40; Mismatches 79; Indels 64; Gaps 10;

QY 41 IRSVLOENRKE-----LAGETPRIVVITSGKGVKTTTANVGLSARVGF 89  
DB 7 VKSKVDAKKEEYNAIRTNIOFSGAQMIAISSVEGEGKSMISVNLAISFASVGLR 66  
QY 90 VVAIDADGLRNLDLLGLENRVNTQVEVINGDCRLDQALVRDKRSMF-----EL 141  
DB 67 TLIDAE--TFN-----SVLSGTFKSNPY--KGLSMFLSGMADLNET 105  
QY 142 LC-----IS-----KPRSKLPMGFGKALEMLVDALKTREGSPDFIITDC-PAG 185  
DB 106 ICQDISGLDVIASGPVPNPFSILQ---NDNFRHLMVARS---CYDYIITDPVPG 157  
QY 186 IDAGFTAITPANEAVALVTPDITLRDADRVLTGLLECGIDIKIMVNRV 236  
DB 158 LVDAVIAIHQADASLVTGAKIRRRVTKAVEQLVESGSGFLGVLVKLV 208

## RESULT 9

US-09-320-878-18  
Sequence 18, Application US/09320878A  
Patent No. 6117659

## GENERAL INFORMATION:

APPLICANT: ASHLEY, Gary  
APPLICANT: BETLACH, Melanie C.  
APPLICANT: BETLACH, Mary C.  
APPLICANT: MCDANIEL, Robert  
APPLICANT: TANG, Li  
TITLE OF INVENTION: RECOMBINANT NARHONOLIDE POLYKETIDE SYNTHASE  
FILE REFERENCE: 300622002120  
CURRENT FILING DATE: 1999-05-27  
EARLIER FILING DATE: 1999-05-27  
EARLIER FILING DATE: 1998-08-28  
EARLIER FILING DATE: 1998-05-06  
EARLIER FILING DATE: 1997-04-30  
EARLIER FILING DATE: 1997-04-30  
EARLIER FILING DATE: 1999-02-08  
EARLIER FILING DATE: 1998-09-22  
EARLIER FILING DATE: 1998-09-22  
EARLIER FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 18  
LENGTH: 416  
TYPE: PRT  
ORGANISM: Streptomyces venezuelae  
US-09-320-878-18

Query Match 5.2%; Score 86.5; DB 3; Length 416;  
Best Local Similarity 22.2%; Pred. No. 0.31;  
Matches 42; Conservative 31; Mismatches 73; Indels 43; Gaps 7;

QY 125 RLDQALVRDKRSMNFELCISKPRSKLPMFGKALEMLVDALKTREGSPDFIITDCPA 184

DB 102 RLKLVAREFTMRVELL---RPVQ-----EIVDGLVAMLAAPDGRADLM----- 145

QY 185 GIDAGFTAITPANEAVALVTPDITLR-----DADRTGLLECCGIDIKMIV 233

DB 146 -ESLAPLPTIVISSELLGVPEPRAAFRVWTDFAVFPDDPAQOTAAKMSGY--LSRLI 202

QY 234 NRVPTDMIKGEDMMSV-----LDVOEMLGLSLGLVPEDESEVIRSTNGFPLVL 282

DB 203 DSKRGQ--DGEDLSALVRSDEDSRLTSEELGMHILLVAGHETVNLANGVYALL 260

QY 283 NKPTIAGL 291  
DB 261 SHPDQALAL 269

## RESULT 10

US-09-105-537-39  
Sequence 39, Application US/09105537A  
Patent No. 6265202

## GENERAL INFORMATION:

APPLICANT: Sherman, D.H.  
APPLICANT: Liu, H.  
APPLICANT: Xue, Y.  
APPLICANT: Zhao, L.  
TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
FILE REFERENCE: 600,438051  
CURRENT FILING DATE: 1998-06-26  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 39  
LENGTH: 416  
TYPE: PRT  
ORGANISM: Streptomyces venezuelae  
US-09-105-537-39

Query Match 5.2%; Score 86.5; DB 4; Length 416;  
Best Local Similarity 22.2%; Pred. No. 0.31;  
Matches 42; Conservative 31; Mismatches 73; Indels 43; Gaps 7;

QY 125 RLDQALVRDKRSMNFELCISKPRSKLPMFGKALEMLVDALKTREGSPDFIITDCPA 184

DB 102 RLKLVAREFTMRVELL---RPVQ-----EIVDGLVAMLAAPDGRADLM----- 145

QY 185 GIDAGFTAITPANEAVALVTPDITLR-----DADRTGLLECCGIDIKMIV 233

DB 146 -ESLAPLPTIVISSELLGVPEPRAAFRVWTDFAVFPDDPAQOTAAKMSGY--LSRLI 202

QY 234 NRVPTDMIKGEDMMSV-----LDVOEMLGLSLGLVPEDESEVIRSTNGFPLVL 282

DB 203 DSKRGQ--DGEDLSALVRSDEDSRLTSEELGMHILLVAGHETVNLANGVYALL 260

QY 283 NKPTIAGL 291  
DB 261 SHPDQALAL 269

## RESULT 11

US-09-085-199B-11  
Sequence 11, Application US/09085199B  
Patent No. 6235879

## GENERAL INFORMATION:

APPLICANT: Hayden, Michael R.  
APPLICANT: Hackam, Abigail  
APPLICANT: Hug, A.H.M. Mahbubul  
APPLICANT: Chopra, Vikramjit Singh  
APPLICANT: Kalchman, Michael  
TITLE OF INVENTION: Apoptosis Modulators That Interact with the  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:

ADDRESS: Opedahl & Larson  
 STREET: PO Box 5270  
 CITY: Frisco  
 STATE: CO  
 COUNTRY: USA  
 ZIP: 80443-5270  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage  
 OPERATING SYSTEM: MS DOS 5.0  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/085,199B  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Larson, Marina T.  
 REGISTRATION NUMBER: 32038  
 REFERENCE/DOCKET NUMBER: UBC-P-013052  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (970) 668-2050  
 TELEFAX: (970) 668-2052  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1068  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: no  
 ORIGINAL SOURCE:  
 ORGANISM: mouse  
 FEATURE:  
 OTHER INFORMATION: Huntington-interacting protein -mH1p1a  
 US-09-085-199B-11

Query Match 5.2%; Score 85.5; DB 4; Length 1068;  
 Best Local Similarity 20.7%; Pred. No. 1.9; Mismatches 69; Conservative 52; Mismatches 147; Indels 65; Gaps 14;  
 Matches 69; Conservative 52; Mismatches 147; Indels 65; Gaps 14;  
 QY 12 QSLLPSSLSOKTLLSPFVNPS-RRSPISRVLOFN-----RKPELAGETPPI 60  
 DB 731 RALEVLQGLDQOYVLRNQ-----PSLMRAPLQIGIQLQGLDLPKSLDVQOELGANVDKE 786  
 QY 61 VVITSGGKGVKTTTANVGLSLARYGSVAIDDLGIRN-----LDLLGLENNY 112  
 DB 787 MAATS--AAIEDAVRIEDMMSOARHSSGVKLEVENRILNCTDLMKAIIRLLVMTSTSL 844  
 QY 113 NYTCVEYINGDCRLDQALVRDRKMSNFELLCISKRSLPMPGFGKALEMLVDALKTRE 172  
 DB 845 QKEIVESGRGATQOEFYAKNSRTE-GLISAK-----AVGWGATQLVESADKVVLLHMG 898  
 QY 173 GSPDFIITDCPAGIDAGTITAITPANEAVALVTPDITALLRADRYTGLLECDGIDIKMI 232  
 DB 899 KYELIIV--CSHEI-----AASQVLVAASKVKANKNSPHLSRLOES--RTVNR 945  
 QY 233 VNRRTMIGEDMSVLDVQEMGLSLGVIPEDSEV-INSTNGCFPLVLLKPPTLAQL 291  
 DB 946 AANVASTKSGQEOIEDRDYDFSLIKLKQEMETQVR-----VLELEKTL--- 994  
 QY 292 AFQAMRLVEODSMKAVM-----EEEPK 317  
 DB 995 --EAERYRLGELRKQHVVLVLAGMGKTPSEEPSR 1025

RESULT 12  
 5223423-2  
 : Patent No. 5223423  
 : APPLICANT: FRANCHINI, GENOVEPPA, WONG-STAAI, FLOOSIE;  
 : GALLO, ROBERT  
 : TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT  
 : HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY  
 : NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/331,212  
 FILING DATE: 03-31-1989  
 SEQ ID NO: 2  
 LENGTH: 3077  
 5223423-2

Query Match 5.0%; Score 83.5; DB 6; Length 3077;  
 Best Local Similarity 21.5%; Pred. No. 17;  
 Matches 61; Conservative 48; Mismatches 122; Indels 53; Gaps 15;  
 QY 57 TPRLVITSGKGVKTTTANVGLSLARYGSVAIDDLGLRNDLLGLENNRYTC 116  
 DB 2037 TPLCVTMNCANSTESAVALTTSQSPDMINDPDCIQLNNCSGLREEDM--VECOFNMG 2093  
 QY 117 VEINGDCRLDQALVRDRKMSNFELLC--ISKPSKLPMPGFGKAL-----EWLVD 165  
 DB 2094 LE-----LDKKQYSTWYSKDYCESDSTDKRCYMNCNVSITESCDKHYW--D 2144  
 QY 166 ALKTRPESGPFITIDCPAGIDAGTITAITPANEAVALVTPDITALLRADRYTGLLECDG 225  
 DB 2145 AMRRYCAPPGFVLLRCNDYVSGF---EPNCSKVAVST--CTRMETQPTWL-----G 2194  
 QY 226 IROIKMIVNRVTD-----MIKGEDMSVLDVQEMGLSLGVIPEDSEVIRST--NRG 277  
 DB 2195 F-----NGRAENRITYYHGRDNRTTISLNKYNLTLICRRPENKTVFTILMSGR 2247  
 QY 278 F--PLVINKPPTLAGLAPEQAMRLVEODSMKAVVEEPPKRG 319  
 DB 2248 FHSQKIINKKPRQAWCRF-KGEMREAME-VKQTLV-KHPRYKG 2288

RESULT 13  
 US-08-416-603-4  
 : Sequence 4, Application US/08416603  
 : Patent No. 5866780  
 : GENERAL INFORMATION:  
 : APPLICANT: Law, Marcus  
 : APPLICANT: Hebara, Ledare  
 : TITLE OF INVENTION: Readdick, Bradford B.  
 : TITLE OF INVENTION: Maize Chlorotic Dwarf Virus Genome and  
 : NUMBER OF SEQUENCES: 11  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Saliwanchik & Saliwanchik  
 : STREET: 2421 N.W. 41st Street, Suite A-1  
 : CITY: Gainesville  
 : STATE: FL  
 : COUNTRY: USA  
 : ZIP: 32606  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: IBM PC compatible  
 : SOFTWARE: Patentin Release #1.0, Version #1.30B  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/416,603  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Lloyd, Jeffrey  
 : REGISTRATION NUMBER: 35,589  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 904-375-8100  
 : INFORMATION FOR SEQ ID NO: 4:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 3457 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-08-416-603-4





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Db 170 IRLNSKP-----PNIGFKKKDKGJNLTFATCPQSELDATVKSILAEYKH-----:11:
OY 98 GLRN-----IDLILGLENRVNYTCVEVINGDCRDLQALVRD-----K 134
Db 220 TLRSDATADLDIDVEG--NRVYIPCIYVLN--KIDQISIEELDIYKVPHCVPISAH 274
OY 135 RWSNEELICISKRPRSKLPMGFGGKALEMLVDALK-----TRPEGS-PDF 177
Db 275 RW-NFDDL-----LEKIMDYLKLVRIYTKPKGQLPDY 305

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Search completed: February 11, 2002, 13:31:36  
 Job time: 23 sec